

1 HOMEBOX

GROWTH ARREST HOMEBOX GENE

BACKGROUND OF THE INVENTION

The leading cause of death in the United States and in most developed countries, is atherosclerosis. Atherosclerosis is a disease affecting the large and medium size muscular arteries such as the coronary or carotid arteries and the large elastic arteries such as the aorta, iliac, and femoral arteries. This disease causes narrowing and calcification of arteries. The narrowing results from deposits of substances in the blood in combination with proliferating vascular smooth muscle cells.

The deposits known as atherosclerotic plaques are comprised of lipoproteins, mainly cholesterol, proliferating vascular smooth muscle cells and fibrous tissue, and extracellular matrix components, which are secreted by vascular smooth muscle cells. As the plaques grow, they narrow the lumen of the vessel decreasing arterial blood flow and weakening the effected arteries. The resulting complications potentially include a complete blockage of the lumen of the artery, with ischemia and necrosis of the organ supplied by the artery, ulceration and thrombus formation with associated embolism, calcification, and aneurysmal dilation. When atherosclerosis causes occlusion of the coronary arteries, it leads to myocardial disfunction, ischemia and infarction and often death. Indeed, 20-25% of deaths in the United States are attributable to atherosclerotic heart disease. Atherosclerosis also leads to lower extremity gangrene, strokes, mesenteric occlusion, ischemic encephalopathy, and renal failure, depending on the specific vasculature involved. Approximately 50% of all deaths in the United States can be attributed to atherosclerosis and its complications.

Present treatments for atherosclerosis include drugs and surgery, including balloon angioplasty. As a result of angioplasty, vascular smooth muscle cells de-differentiate and proliferate and leading to leading to reocclusion of the vessel. These de-differentiated vascular smooth muscle cells deposit collagen and other matrix substances, that contribute to the narrowing of vessel. Vascular cells secrete growth factors such as platelet derived growth factor, which induces both chemotaxis and proliferation of vascular smooth muscle cells.

Many of the present drug therapies treat a predisposing condition such as hyperlipidemia, hypertension, and hypercholesterolemia, in an attempt to slow or halt the progression of the disease. Other drug therapies are aimed at preventing platelet aggregation or the coagulation cascade. Unfortunately, the drug treatments do not reverse existing conditions.

Surgical treatments include coronary artery bypass grafting, balloon angioplasty, or vessel endarterectomy which, when successful, bypass or unblock occluded arteries thereby restoring blood flow through the artery. The surgical treatments do not halt or reverse the progression of the disease because they do not affect smooth muscle cell proliferation and secretion of extracellular matrix components.

The bypass surgeries, particularly the coronary bypass surgeries, are major, complicated surgeries which involve a significant degree of risk. The balloon angioplasty, while also a surgical procedure, is less risky. In balloon angioplasty, a catheter having a deflated balloon is inserted into an artery and positioned next to the plaque. The balloon is inflated thereby compressing the plaque against the arterial wall. As a result, the occlusion is decreased and increased blood flow is restored. However, the balloon

2

angioplasty injures the arterial wall. As a result, the underlying vascular smooth muscle cells migrate to the intima, and synthesize and excrete extracellular matrix components eventually leading to the reocclusion of the vessel. Of the estimated 400,000 coronary artery balloon angioplasties performed each year in the United States, 40% fail due to reocclusion requiring a repeat procedure or coronary bypass surgery. Bypass surgeries also have a significant rate of failure due to internal hyperplasia, which involves excessive proliferation of vascular smooth muscle cells at the sites of vascular anastomoses.

Attempts have been made to prevent reocclusion of vessels after balloon angioplasties in experimental animals. One approach has been to treat rat carotid arteries with antisense oligonucleotides directed against the c-myc gene following balloon angioplasty de-endothelialization. In vascular smooth muscle cells expression of the c-myc gene is up-regulated during the G1 to S transition of the cell cycle, and the activation of c-myc expression is required for further cell cycle progression. The antisense oligonucleotides to c-myc blocked smooth muscle cell proliferation following balloon angioplasty. However, the antisense oligonucleotides are applied in a pleuronic gel to the adventitia, that is, the exterior, rather than the lumen side of the affected vessel. Exposing the exterior of the vessel requires additional surgery with its attendant risks, and is therefore not desirable.

It would be desirable to have a nonsurgical treatment, used in conjunction with balloon angioplasties to reduce vascular smooth muscle cell proliferation.

SUMMARY OF THE INVENTION

A novel growth arrest homeobox gene has been discovered and the nucleotide sequences have been determined in both the rat and the human. The expression of the novel homeobox gene inhibits vascular smooth muscle cell growth. The growth arrest homeobox gene hereinafter referred to as the "Gax gene" and its corresponding proteins are useful in the study of vascular smooth muscle cell proliferation and in the treatment of blood vessel diseases that result from excessive smooth muscle cell proliferation, particularly after balloon angioplasty.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is the nucleotide sequence SEQ. ID. NO. 1 of rat Gax gene with the predicted amino acid sequence SEQ. ID. NO. 2 listed below the nucleotide sequence. The homeobox is indicated by a box, and the CAX nucleotide repeat, where X is either cytosine or guanine, is underlined. A polyadenylation signal is in boldface and italics. Putative consensus sites are indicated as follows: for phosphorylation by protein kinase C, circles; for cyclic AMP (cAMP)-dependent protein kinase, squares; for casein kinase II, diamonds; and for histone H1 kinase, triangles. Residues which could potentially be a target for either cAMP-dependent protein kinase or protein kinase C are both circled and boxed.

FIG. 2 is the map of mouse chromosome 12 showing the location of the Gax gene;

FIG. 3 is the nucleotide sequence SEQ. ID. NO. 3 of human Gax gene with the predicted amino acid sequence SEQ. ID. NO. 4 listed below the nucleotide sequence;

FIG. 4 is a map of human Gax gene showing how the separately cloned fragments were joined and oriented in the plasmid, Bluescript IISK+;

FIG. 5A is a northern blot showing Gax RNA levels in vascular smooth muscle cells in response to 10% fetal calf

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serum after 4, 24, and 48 hours; lane Q is RNA from quiescent cells; GAPDH is rat glyceraldehyde 3-phosphate dehydrogenase;

FIG. 5B is a northern blot showing Gax RNA levels and Hox 1.3 RNA levels in vascular smooth muscle cells in response to 10 ng/ml human platelet derived growth factor at 0.25, 0.5, 1, 2, and 4 hours, lane Q is RNA from quiescent vascular smooth muscle cells;

FIG. 6 is a graph of changes in relative Gax mRNA levels in vascular smooth muscle cells in response to 10% fetal calf serum and 10 mg/ml of the PDGF isoforms; the circles represent PDGF-AA, the squares represent PDGF-BB, the diamonds represent fetal calf serum, and the triangles represent PDGF-AB;

FIG. 7 is a graph showing ³H-thymidine uptake in vascular smooth muscle cells at various times after stimulation with fetal calf serum and PDGF isoforms; the circles represent PDGF-AA, the triangles represent PDGF-AB, the squares represent PDGF-BB, the diamonds represent fetal calf serum, and the solid squares represent no mitogen;

FIG. 8 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to varying doses of PDGF-AB, represented by triangles, and PDGF-BB, represented by squares;

FIG. 9 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to varying doses of fetal calf serum;

FIG. 10 is a graph showing relative Gax mRNA levels in vascular smooth muscle cells in response to fetal calf serum withdrawal;

FIG. 11 is a dose response curve showing % inhibition of growth in vascular smooth muscle cells in response to varying doses of microinjected GST-Gax protein;

FIG. 12 is a graph showing percent inhibition of mitogen induced DNA synthesis in vascular smooth muscle cells in response to: ras (Leu-61) protein; ras (Leu-61) protein in combination with the GST-Gax protein; GST-Gax protein; and the GST;

FIG. 13 is a graph showing percent inhibition of vascular smooth muscle cell entry into S phase by microinjected GST-Gax protein over time and the ³H-thymidine uptake over the same time period;

FIG. 14 is a graph showing the ratio of the Gax mRNA to glyceraldehyde-3-phosphate dehydrogenase designated "G3" level from normal vascular tissue and times following acute blood vessel injury.

DETAILED DESCRIPTION OF THE INVENTION

A novel gene, the Gax gene, has been discovered, the expression of which inhibits vascular smooth muscle cell growth. The Gax gene and the protein it encodes, referred to herein as the "Gax protein" are useful in the study of vascular smooth muscle cell proliferation and in inhibiting smooth muscle cell proliferation. The inhibition of vascular smooth muscle cell proliferation, particularly by genetic therapy, is also useful in the treatment of vascular diseases associated with excessive smooth muscle cell proliferation.

Nucleotide sequences, such as the Gax gene or portions thereof, or mRNA are administered to the vascular cells, preferably during a balloon angioplasty procedure, to inhibit the proliferation of vascular smooth muscle cells. The nucleotide sequences are delivered, preferably to the interior of the vessel wall during balloon angioplasty procedure preferably by a perforated balloon catheter. Genes are transferred

from vectors into vascular smooth muscle cells in vivo where the genes are expressed. Suitable vectors and procedures for the transfer of nucleotides are found in

Nabel, E. G., et al. "Site-Specific Gene Expression in Vivo by Direct Gene Transfer into the Arterial Wall" (1990) *Science* Vol. 249, pp. 1285-1288, which is incorporated herein by reference. Specialized perforated balloon catheters which deliver nucleotide sequences to vessel walls employing viral and non-viral vectors are used for delivery of nucleotide sequences and a description of the catheter's structure and use may be found in Flugelman M. Y., et al. "Low Level In Vivo Gene Transfer Into the Arterial Wall Through a Perforated Balloon Catheter" *Circulation*, Vol. 85, No. 3, pp. 1110-1117 (March 1992) which is incorporated herein by reference.

Genetic therapy, preferably by the over expression of the Gax gene, restores the proliferating vascular smooth muscle cells to a more normal phenotype, thus preventing or reducing the smooth muscle proliferation that is associated with the formation of the atheromatous plaque and with internal arterial thickening following balloon angioplasty. In addition to preventing or reducing the reocclusion of the vessel, such genetic therapy decreases the risks associated with additional surgeries. Also, the Gax proteins or portions thereof, are administered to vascular cells preferably employing the perforated catheter, to inhibit the proliferation of vascular smooth muscle cells.

The molecular control of cellular proliferation is not well understood. A class of genes, known as Homeobox genes, encode a class of transcription factors which are important in embryogenesis, tissue specific gene expression and cell differentiation. The homeobox genes share a highly conserved 183 nucleotide sequence that is referred to as the "homeobox". The homeobox encodes a 61 amino acid helix-turn-helix motif that binds to adenine and thymine rich gene regulatory sequences with high affinity. Several vertebrate homeobox proteins have been shown to be transcription factors required for expression of lineage-specific genes. The tissue-specific transcription factors bind to DNA and repress or induce groups of subordinate genes. Many, but not all of these homeobox genes are located in one of four major clusters known as Hox clusters, designated Hox-1, Hox-2, Hox-3 and Hox-4. The Hox genes are expressed in the developing embryo, in distinct overlapping spatial patterns along the anterior-posterior axis which parallels the Hox gene order along the chromosome. Homeobox transcription factors control axial patterning, cell migration and differentiation in the developing embryo and are involved in the maintenance of tissue specific gene expression in adult organisms.

A new homeobox gene has been discovered, isolated and sequenced in both the rat and human. This new gene is a growth arrest specific homeobox gene and is referred to herein as the "Gax gene". The expression of the Gax gene is restricted to the cardiovascular system, and in particular, to vascular smooth muscle cells where it functions as a negative regulator of cell proliferation.

Isolation of the rat Gax cDNA

An adult rat aorta cDNA library in λ ZAP, from Stratagene, was screened with a 64-fold degenerate 29-mer oligonucleotide containing three inosine residues directed at the most highly conserved region of the antennapedia homeodomain (helix 3), with the following sequence SEQ. ID. NO. 5, where I represents inosine:

5'-AA(A/G)ATTGGTT(T/C)CA(A/G)AA(C/T)(A/C)GI(A/C)
GATGAA-3'.

Recombinant phage colonies in *Escherichia coli* were adsorbed in duplicate to nitrocellulose membranes and hybridized at 42° C. with this oligonucleotide end labeled with (T-32P)ATP in a mixture containing 0.5M sodium phosphate at pH 7.0, 7% sodium dodecyl sulfate, 1 mM EDTA, and 1% bovine serum albumin. The filters were washed with a final stringency of 0.5×SSC (1×SSC in 150 mM NaCl with 15 mM sodium citrate at pH 7.0)–0.1% sodium dodecyl sulfate at 42° C. and exposed to X-ray film. Thirteen positive signals were isolated and rescreened until the clones were plaque purified. The plasmids containing the clones in λ ZAP vector were then excised by the protocol recommended by the manufacturer and sequenced on both strands with sequenase version 2.0 from United States Biochemicals. From 500,000 plaques, 13 positive clones were isolated, 12 of which contained homeodomains. Nine of the isolated clones were derived from previously described homeobox genes: Hox-1.3, Hox-1.4, Hox-1.11, and rat homeobox R1b. However, three clones represented the cDNA designated herein as the "Gax" gene. Homology searches were performed via the GenBank and EMBL data bases, version 73, by using the BLAST algorithm (4).

Nucleotide Sequence of the rat Gax Gene

The nucleotide sequence of the rat Gax gene SEQ. ID. NO. 1 is shown in FIG. 1. The cDNA encoding Gax is 2,244 base pairs in length, which corresponds to the size of the Gax transcript, that is the Gax mRNA, which is about 2.3 to 2.4 kb as determined by Northern blot analysis. The Gax cDNA has an open reading frame from nucleotide residues 197 to 1108 beginning with an in-frame methionine that conforms to the eukaryotic consensus sequence for the start of translation and is preceded by multiple stop codons in all three reading frames. The open reading frame of the cDNA predicts a 33.6-kDa protein SEQ. ID. NO. 2 containing 303 amino acids with a homeodomain from amino acid residues 185 to 245, as shown in FIG. 1. To confirm that this CDNA was capable of producing a protein product, the Gax open reading frame was fused in frame to the pQE-9 *E. coli* expression vector, from Qiagen, Inc., Chatsworth, Calif. and expressed in bacteria according to Hochuli, E., et. al. (1988) "Genetic Approach to Facilitate Purification of Recombinant Proteins with a Novel Metal Chelate Adsorbent" *Bio/Technology* Vol. 6, pp. 1321–1325. *E. coli* containing this plasmid expressed a new protein of about 30 to about 36 kDa as determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and extracts from these *E. coli* cells displayed a weak binding activity for the adenine and thymine rich, MHox-binding site in the creatine kinase M enhancer.

The cDNA encoding the rat Gax gene also contains a long 3'-untranslated region, from bases 1109 to 2244, with a polyadenylation signal at base 2237, as shown in FIG. 1. The region between amino acids 87 and 184 contains 23 serine amino acids out of 88 amino acids and 10 proline amino acids out of 88 amino acids and contains several consensus sequences for phosphorylation by protein kinases. Gax also possesses a structural feature which is also found in several transcription factors, including homeodomain proteins, known as the CAX or Opa transcribed repeat. The Opa transcribed repeat encodes a stretch of glutamines and histidines; in the rat Gax gene it encodes 18 residues, of which 12 are consecutive histidines. This motif is shared by other transcription factors, such as the zinc finger gene YY-1, as well as by several homeobox genes, including H2.0, HB24, ERA-1 (Hox-1.6), Dual bar, and Tes-1. The Gax protein may require post-translational modifications for full activity, modifications that bacterially produced proteins

do not undergo. Since the Gax protein has multiple consensus sites for phosphorylation by protein kinases, it is possible that its activity is activated or otherwise modulated by phosphorylation at one or more of those sites.

The Gax Gene Maps to a Chromosome 12 of the Mouse Genome

Gax is located on chromosome 12 as shown in FIG. 2 of the mouse and is not a part of the Hox-1, Hox-2, Hox-3, or Hox-4 gene clusters, which are located on chromosomes 6, 11, 15, and 2, respectively, McGinnis, W., and R. Krumlauf, (1992) "Homeobox genes and Axial Patterning" Cell, Vol. 68, pp. 283–302. Also Gax does not cosegregate with any other homeobox genes previously mapped in the interspecific backcross. A comparison was done of the interspecific map of chromosome 12 with a composite mouse linkage map that reports the map location of many uncloned mouse mutations using GBASE, a computerized data base maintained at The Jackson Laboratory, Bar Harbor, Me. The Gax gene mapped in a region of the composite map that lacks mouse mutations with a phenotype that might be expected for an alteration in this locus.

The mouse chromosomal location of the Gax was determined by interspecific backcross analysis using progeny generated by mating (C57BL/6J×*Mus spretus*)F₁ females and C57BL/6J males. The C57BL/6J and *M. spretus* DNAs were digested with several enzymes and analyzed by Southern blot hybridization for informative restriction fragment length polymorphisms with a rat cDNA Gax probe. The probe, a 1,155-bp rat cDNA clone, was labeled with (α -³²P) dCTP by using a random prime labeling kit from Amersham and washing was done with a final stringency of 0.2×SSCP (34)–0.1% sodium dodecyl sulfate, 65° C. A major fragment of 4.2 kb was detected in HincII-digested C57BL/6J DNA, and major fragments of 3.6 and 2.7 kb were detected in HincII-digested *M. spretus* DNA. The 3.6-kb and 2.7-kb *M. spretus* HincII restriction fragment length polymorphisms were used to monitor the segregation of the Gax locus in backcross mice. Recombination distances were calculated by using the computer program SPRETUS MADNESS. Gene order was determined by minimizing the number of recombination events required to explain the allele distribution patterns.

The mapping results indicated that the mouse Gax gene is located in the proximal region of mouse chromosome 12 linked to neuroblastoma myc-related oncogene-1 (Nmyc-1), the laminin B1 subunit gene (Lamb-1), a DNA segment, chromosome 12, the Nyu 1 gene (D12Nyu1), and the β -spectrin gene (Spm-1). The ratios of the total number of mice exhibiting recombinant chromosomes to the total number of mice analyzed for each pair of loci and the most likely gene order are as follows: centromere-Nmyc-1-19/193-Lamb-1-9/166-Gax-10/166-D12Nyu1-19/185-Spm-1. The recombination frequencies, expressed as genetic distances in centimorgans±the standard error, are as follows: Nmyc-1-9.8±2.2-Lamb-1-5.4±1.8-Gax-6.0±1.9-D12Nyu1-10.3±2.2-Spm-1.

Gax Gene Expression in Rat Tissue

It has been discovered that the Gax transcript is largely confined to the cardiovascular system, including the descending thoracic aorta, where it is expressed at higher levels than in other tissues, and the heart. Gax gene expression was also detected in the adult lung and kidney where it is found in mesangial cells. No Gax gene expression was detected in the brain, liver, skeletal muscle, spleen, stomach, or testes, nor was expression detected in the intestine or pancreas. In contrast, the Gax gene was more widely expressed in the developing embryo, with the transcript

detectable in the developing cardiovascular system, multiple mesodermal tissues, and some ectodermal tissues.

The 2.3-kb to 2.4-kb Gax RNA transcript was detected in smooth muscle cells cultured from adult rat aorta, consistent with the *in situ* hybridization findings and the fact that Gax was originally isolated from a vascular smooth muscle library. The Gax transcript was also detected in rat vascular smooth muscle cells transformed by simian virus 40. However, no Gax gene expression was detected in either of two cell lines derived from embryonic rat aortic smooth muscle, A7r5 and A10. The Gax transcript was also not detected in NIH 3T3 fibroblasts, or human foreskin fibroblasts. The Gax transcript was not detected in the skeletal muscle cell line C2C12. A relatively high level of Gax gene expression was detected in cultured rat mesangial cells. Mesangial cells share many similarities to vascular smooth muscle cells, both structurally and functionally, and proliferate abnormally in renal diseases such as glomerulonephritis and glomerulosclerosis.

Isolation of the Human Gax cDNA

The nucleotide sequence SEQ. Id. No. 3' of the human Gax gene coding sequence is shown in FIG. 3. Approximately 1×10^6 plaques from a human genomic library in λ FixII available from Stratagene were screened by conventional methods with a random primed EcoRI/BstXI fragment encompassing nucleotides 485-1151 of the rat Gax cDNA. Two clones contained the second exon of human Gax gene, having 182 base pairs. Using this coding information, the rest of the coding region was cloned by polymerase chain reaction methods.

Reverse transcriptase and polymerase chain reaction techniques were used to clone the 3' end of the human cDNA. The template was whole human RNA isolated from human internal mammary artery isolated by TRI reagent from Molecular Research Center, Inc. The following reagent concentrations were used in the reverse transcriptase reaction: 1 μ g of total internal mammary artery RNA; 50 mM Tris-HCl pH 8.5; 30 mM KCl; 8 mM MgCl₂; 1 mM DTT; 20 units RNasin from Boehringer Mannheim; 1 mM each of dATP, dTTP, dGTP, and dCTP; 0.5 μ g random hexamers from Boehringer Mannheim; and 40 u of AMV reverse transcriptase from Boehringer Mannheim, in a total volume of 20 μ L. This was incubated for 1 hour at 42° C., heat inactivated, and then stored at -80° C. before use. An initial amplification of 10% of the reverse transcriptase reaction was performed with just the sense oligonucleotide primer, known as "H2" and Ampliwax™ PCR Gem 100 beads Perkin Elmer in a "hot start" procedure according to the directions of the manufacturer. The following reagent concentrations were used: 50 mM KCL; 10 mM Tris-HCl at pH 8.3; 1.5 mM MgCl₂; 1 mg/mL gelatin; 0.2 mM each of dATP, dTTP, dGTP, and dCTP; 0.1 μ M primer(s); and 2.5 units of Taq polymerase from Boehringer Mannheim or Perkin Elmer in a volume of 100 μ L (these conditions were used thereafter unless noted). The cycling protocol was as follows: 94° C. for two minutes, then 30 cycles of 94° C. for 30 seconds, 45° C. for 1 minute, and 72° C. for 1 minute. A second amplification was then performed on 10% of the primary reaction products using the H2 primer and a degenerate antisense oligonucleotide primer known as "P2B" against the carboxy terminal peptide. The cycling parameters were: 94° C. for two minutes followed by 30 cycles of 94° C. for 30 seconds, 40° C. for 30 seconds, 50° C. for 1 minute and 72° C. for 1 minute. A product was observed of the correct size and following purification by Glass Fog from Bio101, on 2% Biogel agarose from Bio101 was blunt sub-cloned into EcoRV digested BluescriptII SK+ vectors

from Stratagene and sequenced to high resolution by Sequenase 2.0 from universal primers from United States Biochemical. Five individual clones were sequenced to eliminate any spurious Taq polymerase errors.

The 5' end of the human coding region was amplified using an anchored polymerase chain reaction kit, available under the tradename "5'-Amplifinder RACE" from Clontech according to the manufacturer's instructions. This method uses single stranded RNA ligase to ligate an anchor oligonucleotide onto the 3' end of appropriately primed first strand cDNA. Templates used were either human heart polyA+ RNA obtained from Clontech or polyA+ RNA isolated from primary cultures of human vascular smooth muscle cells obtained from Clontech. The polyA+ RNA from cultured vascular smooth muscle cells was purified with RNazol B from Biotex using batch chromatography on Oligo-dT latex beads from Qiagen. Both templates yielded amplified cDNAs and specific subclones were chosen solely by size. First strand RNA templates were prepared by either specific priming or priming with random hexamers from Boehringer Mannheim. In general, the specific primed templates yielded longer clones but could not be used for multiple step wise amplification of the rest of the coding region.

Amplification from anchored templates using the sense anchor primer and appropriate antisense specific primers was accomplished using ampliwx beads from Perkin Elmer and "hot start" polymerase chain reaction using the same reaction conditions as above, but with 0.2 μ M primers in a total volume of 50 μ L. The cycling protocol was as follows: 94° C. for 2 minutes then 30 cycles of 94° C. 45 seconds, 60° C. 45 second, and 72° C. for 1.5 minutes, followed by a final extension of 72° C. for 10 minutes. Following a primary amplification, aliquots (10-20%) of the reactions were run out on 2% Biogel agarose from Bio101 and size selected. After purification by glass fog from Bio101, 1-10% of the elutes were reamplified (2°), usually with a nested primer. Products were observed at this point and purified by glass fog as before and sequenced directly using a thermal cycling kit from New England Biolabs. Once the products were confirmed they were sub-cloned as described above. Between 5 to 8 individual clones from each of three sequential amplifications were sequenced to eliminate spurious Taq polymerase errors and appropriate clones chosen for the finished molecule. A summary of the primer pairs sense/antisense used to amplify the complete coding region:

position	Clone #	Source of Template	1°	2°	5'-3'
6	dN6 primed	IMA whole RNA	H2	H2/P2B	699-941
23	H2R primed	Heart polyA + RNA	AP/H2R	AP/H3	231-693
117	dN6 primed	VSMC poly A + RNA	AP/H6	AP/H6	119-230
131	dN6 primed	VSMC poly A + RNA	AP/H6	AP/H7	1-118

Clones were pieced together 3'-5' as follows: fragments 6 and 23 share engineered BglII sites; fragments 23 and 117 share a native SfaNI site; fragment 117 has a native NcoI site which is compatible with an engineered BspHI site in fragment 131. Both engineered sites have a single base change in the wobble base of leucine codons, as noted on the final sequence as shown in FIG. 3. Once assembled the molecule was excised by digestion with EcoRI and HindIII. The map in FIG. 4 shows the molecule and its orientation. The DNA molecule was deposited with the American Type

Culture Collection, 12301 Parklawn Drive, Rockville, Md. 20852, on Nov. 24, 1997, and was assigned Accession Number ATCC 209497.

mRNA was extracted. The total RNA from rat cultured cells was prepared by the guanidine thiocyanate method according to Chomczynski, P., and N. Sacchi, (1987) "Single-step

TABLE 1

Primers Used to Amplify Human Gax gene	
Primer	Sequence 5'-3'
P2B SEQ. Id. No. 6	TCA,IA(G/A),(G/A)TG,IGC,(G/A)TG,(T/C)TC
H2 SEQ. Id. No. 7	GCGCGC(AGATCT)CAC,TGA,AAAG,ACA,GGT,AAA
H2R SEQ. Id. No. 8	TT,TAC,CTG,TCT,TTT,AGT,GAG
H3 SEQ. Id. No. 9	GCGCGC(AGATCT)AG,ATT,CAC,TGC,TAT,CTC,GT
H6 SEQ. Id. No. 10	GCGCGTGCCCGCTGATC,CTG,GCT,GGC,AAA,CAT,GT
H7 SEQ. Id. No. 11	GCGCGC(TCTTGA)AGG,GCG,AGA,GAG,GAT,TGG,GA
AP SEQ. Id. No. 12	CTGGTTCCGCCACCTCTGAAGGTTCCAGAATCGATAG
Anchor SEQ. Id. No. 13	GGAGACTTCCAAGGTCTTAGCTATCA(CTTAAG)CAC

Engineered enzyme sites are bracketed.

The Gax gene maps to a novel locus on Chromosome 7 in the human genome

To determine the map location of Gax in the human genome, a 16.5 kilobase pair fragment of the human genomic Gax gene in λ Fix II from Stratagene was purified with a Qiagen purification column according to the directions of the manufacturer, and it was labeled with biotin 11-dUTP by nick translation. Metaphase spreads of normal human lymphocytes were prepared according to the methods of Fan, Y., *Proc. Natl. Acad. Sci. (USA)* Vol. 87, pp. 6223-6227 (1990). Fluorescence in situ hybridization and immunofluorescence detection were performed according to the methods of Pinkel, D., et. al., *Proc. Natl. Acad. Sci. (USA)* Vol. 83, pp. 2934-2938 (1986) and Testa, J. R., et al. *Cytogenet. Cell. Genet.* Vol. 60, pp. 247-249 (1992). Chromosome preparations were stained with diaminido-2-phenylindole and propidium iodide according to Fan, Y. S., et. al., *Proc. Natl. Acad. Sci. (USA)* Vol. 87, pp. 6223-6227 (1990).

Forty metaphase spreads were examined with a Zeiss Axiophot fluorescence microscope, and fluorescent signals were detected on the short arm of chromosome 7 in 34 of these spreads. All signals were located at p15-->p22, with approximately 70% of the signals at 7p21. Based on these data, Gax is the only homeoprotein known to map to this locus.

Gax gene expression is down-regulated in cultured vascular smooth muscle cells upon mitogen stimulation

It has been found that the Gax gene is expressed in quiescent vascular smooth muscle cells. Since platelet derived growth factor hereinafter also referred to as "PDGF" and other growth factors regulate vascular smooth muscle proliferation and differentiation, differences in Gax gene expression in response to PDGF and other mitogens such as fetal calf serum were examined in cultured vascular myocytes.

Cultures of rat smooth muscle cells were obtained from the media of aortas isolated from adult male Sprague-Dawley rats. Cells were seeded onto dishes in medium containing a 1:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 and supplemented with 10% newborn calf serum. Once established, the cells were maintained at 37° C. in a humidified atmosphere of 5% carbon dioxide, and subcultured within three days after reaching confluence. Vascular smooth muscle cells were labeled with monoclonal antibodies to smooth muscle α -actin from Sigma Chemical Co. to verify identity.

The cultured cells were exposed to various mitogens as discussed below. The cells were then harvested and the total

Method of RNA Isolation by Acid Guanidinium Thiocyanate-phenol-chloroform Extraction" *Anal. Biochem.* Vol. 162, pp. 156-159, fractionated on 1.2% agarose gels containing formaldehyde, and blotted onto nylon membranes. The RNA from cultured cells was separated on 30-cm gels for transcript size determination and on 10-cm gels for other studies. Hybridizations were carried out at 65° C. in buffer containing 0.5M sodium phosphate at pH 7.0, 7% sodium dodecyl sulfate, 1 mM EDTA, and 1% bovine serum albumin, using a cDNA probe labeled by random priming consisting of a truncated Gax cDNA lacking the 5' end and the CAX repeat, where the X may be cytosine or guanine. Probes for Hox-1.3 and Hox-1.4 consisted of the cDNAs isolated from the rat aorta library, and the probe for Hox-1.11 consisted of the Dral-EcoRI fragment of its cDNA. The blots were washed with a final stringency of 0.1 to 0.2xSSC-0.1% sodium dodecylsulfate at 65° C. After the probings with the homeobox probes were complete, the blots were rehybridized with a probe to rat glyceraldehyde 3-phosphate dehydrogenase hereinafter also referred to as "GAPDH," to demonstrate message integrity. Gax mRNA and GAPDH mRNA were quantified with a Molecular Dynamics model 400S PhosphorImager to integrate band intensities, or by scanning densitometry of autoradiograms. In all quantitative comparisons of Gax mRNA levels between experimental groups, Gax mRNA levels were normalized to the corresponding GAPDH level determined on the same blot, to account for differences in RNA loading. Time Course of GAX Down-regulation in Cultured Vascular Smooth Muscle Cells

Rat vascular smooth muscle cells, grown to a greater than about 90% confluence, were placed in low-serum medium containing 0.5% calf serum for 3 days, to induce quiescence. At this time, the medium was removed from the cells and replaced with fresh medium containing either 10% fetal calf serum or 10 ng/ml platelet derived growth factor from human platelets. The cells were then incubated for the various times in the presence of either the fetal calf serum or the PDGF. As a control, quiescent cells were incubated with fresh serum-free medium alone. The cells exposed to PDGF were harvested at 0.25, 0.5, 1, 2, and 4 hours, and the cellular RNA isolated. The cells exposed to human fetal calf serum were harvested at 4, 24, and 48 hours. The Gax and the Hox mRNA levels were determined by Northern blot analysis. Typical results are shown in FIGS. 5A and 5B.

A rapid down-regulation, that is a reduction in the amount of Gax mRNA, occurred in the vascular smooth muscle cells when they were stimulated with either fetal calf serum or

12

As shown in FIG. 8, the dose response curves reveal that the 50% effective dose for Gax gene down-regulation 4 hours after PDGF-AB stimulation is between 4 and 8 ng/ml. The 50% effective dose for Gax gene down regulation 4

To produce the Gax protein evaluated herein, the cDNA coding regions for Gax was fused in frame to the pGEX-2T expression vector obtained from Pharmacia Biotechnology, and then expressed in *E. coli*. Specifically, GST-Gax was produced according to the following procedure: the coding region of Gax cDNA spanning from nucleotides 200–1108 was amplified by polymerase chain reaction methods using the following primers:

The resulting DNA was digested with Sall and HindIII restriction enzymes and cloned into Sall and HindIII sites in the polylinker of pGEM3-IT in vitro transcription translation vector described in Patel R. C. and Sen G. C. (1992) "Identification of the Double-stranded RNA-binding

Domain in the Human Interferon-inducible Protein Kinase," *J. Biol. Chem.* Vol. 267, pp. 7671-7676. The BamHI to NaeI fragment of pGEM3-IT containing the Gax coding region was then sub-cloned into the same sites of pGEX-2T. The pGEX-2T vector with the YY1 cDNA, used to produce GST-YY1, was from Thomas Shenk at Princeton University.

The resultant glutathione S-transferase fusion proteins were purified by affinity chromatography on glutathione-agarose beads. *E. coli* XL1-blue cells were then transformed with the appropriate plasmid and were grown to a density of 0.6-0.8 A₅₀₀ and induced with 0.5 mM isopropyl-B-D-thiogalactopyranoside for 2 hours. The cells were harvested and lysed by ultrasonic vibration in phosphate buffered saline containing 1% triton x-100, 1 mM PMSF and 5 µg/ml aprotinin. The lysate was centrifuged at 15,000xg and the supernatant was collected. The supernatant was bound to the glutathione sepharose from Pharmacia (0.5 ml of resin per 100 ml of bacterial culture) for 2 hours on a rotator at 25 rpm. The slurry was pelleted by centrifugation at 1000xg for 2 minutes, then washed twice with complete lysis buffer then washed twice with lysis buffer lacking triton x-100. The bound protein was eluted for 30 minutes with phosphate buffered saline containing 10 mM reduced glutathione, from Sigma Chemical Company, 40 mM DTT and 150 mM NaCl. Purity of the GST-Gax protein was greater than 90% as determined by SDS-PAGE gels stained with Coomassie blue.

To produce recombinant MHox, its cDNA was fused in frame to the pQE-9 *E. coli* expression vector obtained from Qiagen, Inc., Chatsworth, Calif., then expressed in bacteria, and purified by adsorption to a nickel column.

For microinjection, proteins were concentrated in a buffer containing of 20 mM Tris, 40 mM KCl, 0.1 mM EDTA, 1 mM β-mercaptoethanol, and 2% glycerol using Centricon-30 from Amicon microconcentrators. Concentrated proteins were stored in this buffer in aliquots at -80° C.

Microinjection and Cell Culture Methods

Microinjections were performed using a semiautomatic microinjection system from Eppendorf Inc. in conjunction with a Nikon Diaphot phase contrast microscope. According to Peperkole, R., et al. (1988) *Proc. Natl. Acad. Sci. USA* Vol. 85, pp. 6758-6762, The injection pressure was set at 70-200 hPa and the injection time was 0.3 to 0.6 seconds.

After injection, cells were stimulated 24 hours with medium containing 10% fetal calf serum, and the incorporation of 5'-bromo-2'-deoxyuridine, hereinafter also referred to as "BrdU" was measured with a cell proliferation kit according to the directions of its manufacturer, Amersham. When fetal calf serum-stimulated BrdU labeling was determined, BrdU was included for 24 hours with the medium used to stimulate the cells. Where the ability of microinjected proteins to stimulate growth in serum-poor medium was measured, cells were incubated 24 hours in the same low serum medium used to induce quiescence, but supplemented with BrdU. After labeling, the cells were fixed with acid-ethanol, and the percentage of nuclei positive for BrdU uptake was determined for protein-injected and buffer-injected cells. The percent of cell growth inhibition was calculated according to the following formula:

$$\% \text{ Inhibition} = \frac{\frac{CL}{CT} - \frac{IL}{IT}}{\frac{CL}{CT}} \times 100$$

where IL represents the number of injected labeling positive for BrdU; IT, the total number of injected cells; CL the number of control-injected cells labeling with BrdU; CT, the

total number of control-injected cells counted. With this equation, inhibition of mitogen-induced entry into S phase is represented by a positive number and stimulation of cell growth is represented by a negative number.

Evaluation of Gax Protein

To determine if the Gax protein inhibits the entry of mitogen stimulated vascular smooth muscle cells into S-phase, the effect of the Gax protein was compared to proteins known to effect cell proliferation, and to control proteins. Such comparison proteins include a neutralizing antibody against ras, "Y13-259," which is highly effective in blocking S phase entry when microinjected into NIH3T3 cells; the transcription factor MHox, a homeodomain protein unlikely to have an inhibitory effect on cell proliferation; and YY1, a zinc finger transcription factor unlikely to have a negative effect on cell growth.

Quiescent rat vascular smooth muscle cells were microinjected with either 0.6 mg/ml GST-Gax protein; 1.6 mg/ml MHox; 1.2 mg/ml YY1; 8 mg/ml Y13-259; 2 mg/ml GST alone; or 8 mg/ml mouse anti-human IgG. The cells were then stimulated for 24 hours with 10% fetal calf serum in medium containing BrdU. After 24 hours, the fraction of nuclei labeling with BrdU was determined and percentage inhibition of S-phase entry calculated. The results are summarized in Table 2.

TABLE 2

Effect of Microinjected Proteins on the Serum-induced Proliferation of Vascular Smooth Muscle Cells

Treatment	Number of Experiments	Total Number of Cells Examined	Mean % Inhibition of FCS-stimulated Growth ± Standard Error
Antibody Y13-259	2	328	60.8 ± 3.9
Mouse anti-human IgG	3	330	-3.4 ± 4.5
GST-Gax	15	2943	42.7 ± 3.3
MHox	2	236	-5.3 ± 9.3
GST-YY1	5	306	0.0 ± 12.2
GST	7	1144	-2.6 ± 2.1

FCS — fetal calf serum

BrdU labeling of quiescent vascular smooth muscle cells was 10.1 ± 1.2% (N = 12, total number of cells counted = 2659); for uninjected FCS-stimulated vascular smooth muscle cells, 54.8 ± 2.4% (N = 27, total number of cells counted = 4282); and for sham-injected FCS-stimulated cells, 49.6 ± 2.5% (N = 27, total number of cells injected = 3401).

As shown in Table 2, the GST-Gax protein inhibited vascular smooth muscle cell entry into S-phase by 42.7%. The GST Gax protein effect on mitogen-stimulated entry into S phase is specific. The other injected proteins GST, YY1, MHox and the mouse anti-human IgG failed to inhibit vascular smooth muscle cell growth. In comparison to the GST-Gax protein, the antibody Y13-259, as anticipated, significantly decreased mitogen-induced cell proliferation. Vascular smooth muscle cells microinjected with Y13259 demonstrated a 61±4% decrease in cell entry into S-phase. Gax Protein Inhibits Vascular Smooth Muscle Cell Proliferation in a Dose-Dependent Manner.

To determine the concentration of microinjected GST-Gax required to inhibit vascular smooth muscle cell growth, solutions containing different concentrations of GST-Gax protein were microinjected into quiescent vascular smooth muscle cell and the effects on mitogen-stimulated entry into S phase examined. Specifically, vascular smooth muscle cells were rendered quiescent by incubation in medium containing 0.5% calf serum for three days. The cells were microinjected with varying concentrations of GST-Gax, and stimulated with 10% fetal calf serum, and labeled with

BrdU. After 24 hours, the percentage inhibition of cell proliferation was determined. Each data point represents the mean \pm standard error of 3–5 experiments in which 100–200 cells per experimental group were injected.

As shown in FIG. 11, the cellular growth inhibition by the GST-Gax protein is dose dependent. Little or no growth inhibition was observed when 0.2 mg/ml GST-Gax protein was injected. The maximal growth inhibition was obtained with approximately 0.5 mg/ml of the GST-Gax protein.

Gax Inhibits Proliferation of Several Cell Types

To determine whether the GST-Gax protein inhibits growth in other cell types, the GST-Gax protein was microinjected into quiescent SV40-transformed vascular smooth muscle cells, BALB/c3T3 cells, NIH3T3 cells, human vascular smooth muscle cells, and human fibroblasts. The SV40 transformed cell line was derived from rat vascular smooth muscle cells transformed with the SV40 large T antigen. These cells, while immortalized, retain many differentiated characteristics of untransformed vascular smooth muscle cells. The cells were microinjected with either 0.6 mg/ml GST-Gax protein or 2 mg/ml GST were then stimulated with 10% fetal calf serum, and labeled for 24 hours with BrdU. The results are shown in Table 3.

TABLE 3

EFFECT OF MICROINJECTED GST-GAX PROTEIN ON CELL PROLIFERATION IN DIFFERENT CELL TYPES

Cell type	GST-GAX protein	Number of Experiments	Number of Cells Examined	Mean & Range Inhibition of FCS-Stimulated Growth	Mitotic Index in Response to FCS
SV40-transformed VSMC	Yes	4	448	27.2 \pm 2.0	—
SV40-transformed VSMC	No			N/A	0.60 \pm 0.02
BALB/c 3T3 cells	Yes	4	464	30.5 \pm 10.9	—
BALB/c 3T3 cells	No			N/A	0.64 \pm 0.03
NIH3T3 cells	Yes	4	420	23.2 \pm 1.8	—
NIH3T3 cells	No			N/A	0.70 \pm 0.02
Human VSMC	Yes	3	506	46.6 \pm 8.1	—
Human VSMC	No			N/A	0.33 \pm 0.02
Human fibroblasts	Yes	3	336	44.5 \pm 2.1	—
Human fibroblasts	No			N/A	0.36 \pm 0.01

FCS — fetal calf serum

VSMC — vascular smooth muscle cells

SV40—transformed vascular smooth muscle cell proliferation was inhibited by GST-Gax protein, as shown in Table 3. The GST-Gax protein also inhibited the proliferation of fibroblast cell lines NIH3T3 and BALB/c 3T3. GST-Gax protein also inhibited the proliferation of human cells, specifically human vascular smooth muscle cells and human foreskin fibroblasts. These results indicate that Gax action is not cell type-specific, although there are differences in the extent inhibition among the different cell types. Among the human cells, the GST-Gax protein exhibits maximal inhibition in vascular smooth muscle cells, the cell type in which the Gax gene is normally expressed. Similarly among the rat cells, the GST-Gax protein exhibits maximal inhibition in vascular smooth muscle cells, the cell type in which the Gax gene is normally expressed.

An Oncogenic Ras Protein Can Reverse Growth Inhibition Caused by the Gax protein

To characterize the mechanism of the growth inhibition conferred by the GST-Gax protein, the effects of GST-Gax protein and the transforming oncoprotein, the ras mutant Ras(Leu-61) were compared by microinjecting these proteins into rat vascular smooth muscle cells. A solution containing both 0.5 mg/ml GST-Gax protein and 0.5 mg/ml Ras(Leu-61) was microinjected into quiescent vascular smooth muscle cells. For comparison, other vascular smooth muscle cells received either 0.5 mg/ml GST-Gax protein or 0.5 mg/ml Ras(Leu-61) or 0.5 mg/ml GST. The injected cells were then incubated for 24 hours with medium containing 10% fetal calf serum and BrdU. The results are shown in FIG. 12.

As shown in FIG. 12, when Ras(Leu-61) alone was injected, there was an increase in BrdU-labeling as compared to both control-injected cells. In cells injected with GST-Gax protein, growth was inhibited 39%. When the GST-Gax protein and Ras(Leu-61) were coinjected in the cells, the Ras(Leu-61) reversed the growth inhibitory effects of the GST-Gax protein, and the percentage of cells staining positive for BrdU in cells receiving both the Ras(Leu-61)

and GST-Gax protein were nearly identical to that observed in cells receiving just the Ras(Leu-61). Thus, the Ras oncoprotein completely reversed the effect of the GST-Gax protein establishing that the presence of GST-Gax protein is not toxic to cells.

The Gax Protein Inhibits Cell Growth when Microinjected Before the G1 to S Boundary

To determine the point in the cell cycle when the Gax gene exerts its growth inhibitory effects, the time of S phase onset was determined in rat vascular smooth muscle cells. The vascular smooth muscle cells were stimulated with 10% fetal calf serum and pulse labeled with 10 mCi/ml ³H-thymidine for one hour at different times after stimulation. Separate cultures of the cells were microinjected with GST-Gax protein at various times after receiving 10% fetal calf serum and labeled with BrdU between 10 and 24 hours

after receiving the fetal calf serum. Percent inhibition of S-phase entry was determined at each time point. The results are shown in FIG. 13.

As shown in FIG. 13, S phase onset, indicated by the uptake of ^3H -thymidine, occurred at approximately 16–18 hours after mitogen stimulation. GST-Gax protein significantly inhibited vascular smooth muscle cell entry into the S phase when microinjected at any time from stimulation up until approximately 12 hours. However, GST-Gax protein was ineffective when injected at 15 hours. Thus it appears that the Gax gene inhibits a critical step in cell cycle progression prior to the G₁/S boundary; perhaps before the restriction point in G₁, where eukaryotic cells are irreversibly committed to entering the S phase.

Gax Gene Expression is Rapidly Down Regulated in Vivo Upon Acute Blood Vessel Injury

The Gax gene expression in normal blood vessels and in injured blood vessels was compared to determine whether Gax gene down-regulation occurs in response to injury-induced smooth muscle cell proliferation in vivo. Adult male Sprague-Dawley rats were subject to acute vessel injury by balloon de-endothelialization in the carotid arteries according to the methods of Majesky, M. W., et al. *J. Cell Biol.* (1990) Vol. 111, pp. 2149–2158. The expression levels of Gax, that is, the mRNA levels, were assessed relative to that of glyceraldehyde 3-phosphate dehydrogenase (hereinafter also referred to as "G3") by a quantitative polymerase chain reaction. At various times following balloon de-endothelialization the rats were sacrificed and the total RNA was isolated from the vascular smooth muscle tissues using the TRI reagent from Molecular Research Center, Inc. The cDNA was synthesized from the extracted RNA with MMLV reverse transcriptase from Bethesda Research Labs. Aliquots of the cDNA pools were subjected to polymerase chain reaction amplification with AmpliTaq DNA polymerase from Perkin-Elmer in the presence of a32P-dCTP with the following cycle conditions: 94° C. for 20 seconds, 55° C. for 20 seconds, and 72° C. for 20 seconds. The final cycle had an elongation step at 72° C. for 5 minutes. The primers for the rat Gax amplification were: 5'-CCCGCGCGGCTTTTACATTAGGAGT-3' SEQ. Id. NO. 16 and 5'-GCTGGCAAAACATGCCCTCCTCATTG-3' SEQ. Id. NO. 17. The primers for the rat G3 gene were 5'-TGATGGCATGGACTGTGGTCATGA-3' SEQ. Id. NO. 18 and 5'-TGATGGCATGGACTGTGGTCATGA-3' SEQ. Id. NO. 19. The Gax cDNA was amplified for 30 cycles, and G3

was amplified for 25 cycles in the same reaction vessels. The amount of a radioactive label incorporated into the amplified cDNA and G3 fragments was determined by subjecting the fragments to electrophoresis on a 1% agarose gel, then excising the bands and liquid scintillation counting. Since the mRNA levels of glyceraldehyde 3-phosphate dehydrogenase remain relatively constant following this procedure (see J. M. Miano et al. 1990, *Am. J. Path.* 137, 761–765), the ratio of radiolabel incorporation into the Gax-derived amplified bands and the G3-derived amplified bands corrects for differences arising from the efficiency of RNA extraction from the different animals, and it provides a measure of Gax mRNA levels in the normal and injured vascular tissues. These ratios are plotted in FIG. 14.

As shown in FIG. 14, the Gax mRNA expression was down-regulated in response to acute vessel injury by as much as a factor of 20. This down-regulation was rapid and appeared complete by 2 hours, the first time-point following the de-endothelialization procedure. Collectively, these data corroborate the Gax gene down-regulation in cultures of vascular smooth muscle cells following growth factor stimulation. Further, these data show that Gax gene expression is an early marker of the cell cycle activity associated with the initiation of vascular restenosis, and they indicate that Gax has a regulatory role following blood vessel injury.

The present invention includes: the DNA sequences encoding a protein, or portion thereof, which inhibits vascular smooth muscle cell proliferation; the messenger RNA transcript of such DNA sequence; and an isolated protein which inhibits vascular smooth muscle cell growth.

For example, the DNA sequences include: DNA molecules which, but for the degeneracy of the genetic code would hybridize to DNA encoding the Gax protein, thus the degenerate DNA which encodes the Gax protein; DNA strands complementary to DNA sequences encoding the Gax protein or portions thereof including DNA in FIGS. 1 and 3 or portions thereof; heterologous DNA having substantial sequence homology to the DNA encoding the Gax protein, including the DNA sequences in FIGS. 1 and 3 or portions thereof.

The isolated protein includes, for example, portions of the Gax protein; the Gax protein of animals other than rat and human; and proteins or portions thereof having substantially the same amino acid sequence as shown in FIGS. 1 and 3 or portions thereof.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(1.1) NUMBER OF SEQUENCES: 19

(2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: cDNA

(1.1.1) HYPOTHETICAL: NO

(1.1.2) ANTI-SENSE: NO

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(1x) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 197..1108

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGTGAAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGAAG      180
CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC      229
      Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
      1          5          10

CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG      277
Pro His Ala Thr Ala Glu Gly Leu His Pro Phe Ser Glu Ser Ser Leu
      15          20          25

GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA      325
Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
      30          35          40

TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG      373
Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
      45          50          55

TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC      421
Phe Ala Ser Glu His His Arg Gly His His His His His His His
      60          65          70          75

CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG      469
His His His His Glu Glu Glu Glu His Glu Ala Leu Glu Ser Asn Trp
      80          85          90

CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT      517
His Leu Pro Glu Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
      95          100          105

TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT      565
Cys Leu Glu Pro Asp Ser Gly Gly Pro Pro Pro Glu Leu Gly Ser Ser Pro
      110          115          120

CCG GTC CTG TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC      613
Pro Val Leu Cys Ser Asn Ser Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr
      125          130          135

GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA GCG CTG TCA CCC      661
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      140          145          150          155

GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA      709
Ala Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser
      160          165          170

GAT TCC CAG GAA GGA AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG      757
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      175          180          185

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      190          195          200

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      205          210          215

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Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Glu Glu Gly Ala
      240          245          250

GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT      997
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285 290 295	
CAC GCA CAC TTA TGATACATAC AGAGACCAGC TCCGTTCTCA GGAAAGCACC	1145
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TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC	1925
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GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAAACTG TTAATGGTAT GTGTCTGCTT	2045
CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA	2105
CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA	2165
AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA	2225
AAAAAAAGTT AAATAAATG	2244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Glu	Gly	Leu	His	Pro	Phe	Ser	Glu	Ser	Leu	Ala	Leu	His	Gly	Arg		20	25	30	
Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	35	40	45	
Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Glu	Glu	Gly	Met	Phe	Ala	Ser	Glu	His	50	55	60	
His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Glu	65	70	75	80
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Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Glu	Pro	Asp
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Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala
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Pro	Arg	Asp	Tyr	Gly	Arg	Glu	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys
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Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Glu	Glu	Gly
				165					170					175	
Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Arg	Glu	Arg	Thr	Ala
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Phe	Thr	Lys	Glu	Glu	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His
		195					200					205			
Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp
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Leu	Thr	Glu	Arg	Glu	Val	Lys	Val	Trp	Phe	Glu	Asn	Arg	Arg	Met	Lys
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Trp	Lys	Arg	Val	Lys	Gly	Gly	Glu	Glu	Gly	Ala	Ala	Ala	Arg	Glu	Lys
				245					250					255	
Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser
			260					265					270		
Gly	Ile	Gly	Ala	Ala	Thr	Leu	Glu	Glu	Thr	Gly	Asp	Ser	Leu	Ala	Asn
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(2) INFORMATION FOR SEQ ID NO-3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(i v) ANTI-SENSE: NO

(i x) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 33_941

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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				1				5								
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Cys	Leu	Arg	Ser	Pro	His	Ala	Thr	Ala	Gln	Gly	Leu	His	Pro	Phe	Ser	
		10					15					20				
CAA	TCC	TCT	CTC	GCC	CTC	CAT	GGA	AGA	TCT	GAC	CAT	ATG	TCT	TAC	CCC	149
Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg	Ser	Asp	His	Met	Ser	Tyr	Pro	
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Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	Ile	Ile	Ala	Gly	Tyr	Pro	Asn	
40					45				50						55	
GAA	GAG	GAC	ATG	TTT	GCC	AGC	CAG	CAT	CAC	AGG	GGG	CAC	CAC	CAC	CAC	245
Glu	Glu	Asp	Met	Phe	Ala	Ser	Gln	His	His	Arg	Gly	His	His	His	His	
				60					65					70		

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26

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CAC	CAC	CAC	CAT	CAC	CAC	CAT	CAG	CAG	CAG	CAG	CAC	CAG	GCT	CTG	CAA	293
His	His	His	His	His	His	His	Gln	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	
			75				80						85			
ACC	AAC	TGG	CAC	CTC	CCG	CAG	ATG	TCT	TCC	CCA	CCG	AGT	GCG	GCT	CGG	341
Thr	Asn	Trp	His	Leu	Pro	Gln	Met	Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	
		90					95					100				
CAT	AGC	CTC	TGC	CTC	CAG	CCC	GAC	TCT	GGA	GGG	CCC	CCA	GAG	TTG	GGG	389
His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	
	105					110					115					
AGC	AGC	CCG	CCC	GTC	CTG	TGC	TCC	AAC	TCT	TCC	AGC	TTG	GGC	TCC	AGC	437
Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	Asn	Ser		Ser	Ser	Leu	Gly	Ser	
120				125						130					135	
ACC	CCG	ACT	GGG	GCC	GCG	TGC	GCG	CCG	GGG	GAC	TAC	GGC	CGC	CAG	GCA	485
Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	Pro	Gly	Asp	Tyr	Gly	Arg	Gln	Ala	
				140					145					150		
CTG	TCA	CCT	GCG	GAG	GCG	GAG	AAG	CGA	AGC	GGC	GGC	AAG	AGG	AAA	AGC	533
Leu	Ser	Pro		Glu	Ala	Glu	Lys	Arg	Ser	Gly	Gly	Lys	Arg	Lys	Ser	
			155				160						165			
GAC	AGC	TCA	GAC	TCC	CAG	GAA	GGA	AAT	TAC	AAG	TCA	GAA	GTC	AAC	AGC	581
Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	
		170					175					180				
AAA	CCC	AGG	AAA	GAA	AGG	ACA	GCA	TTT	ACC	AAA	GAG	CAA	ATC	AGA	GAA	629
Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Gln	
	185					190					195					
CTT	GAA	GCA	GAA	TTT	GCC	CAT	CAT	AAT	TAT	CTC	ACC	AGA	CTG	AGG	CGA	677
Leu	Glu	Ala	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	
200				205						210				215		
TAC	GAG	ATA	GCA	GTG	AAT	CTG	GAT	CTC	ACT	GAA	AGA	CAG	GTA	AAA	GTC	725
Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp	Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	
				220					225					230		
TGG	TTC	CAA	AAC	AGG	CGG	ATG	AAG	TGG	AAG	AGG	GTA	AAG	GGT	GGA	CAG	773
Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	
			235				240						245			
CAA	GGA	GCT	GCG	GCT	CGG	GAA	AAG	GAA	CTG	GTG	AAT	GTG	AAA	AAG	GGA	821
Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys	Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	
		250				255						260				
ACA	CTT	CTC	CCA	TCA	GAG	CTG	TCG	GGA	ATT	GGT	GCA	GCC	ACC	CTC	CAG	869
Thr	Leu	Leu	Pro	Ser	Gln	Leu	Ser	Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	
	265					270					275					
CAA	ACA	GGG	GAC	TCT	ATA	GCA	AAT	GAA	GAC	AGT	CAC	GAC	AGT	GAC	CAC	917
Gln	Thr	Gly	Asp	Ser	Ile	Ala	Asn	Glu	Asp	Ser	His	Asp	Ser	Asp	His	
280				285					290						295	
AGC	TCA	GAG	CAC	GCC	CAC	CTC	TGA									941
Ser	Ser	Glu	His	Ala	His	Leu										
				300												

(2) INFORMATION FOR SEQ ID NO:4:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
 1 5 10 15

Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
 20 25 30

Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys
 35 40 45

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Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Glu His
  50          55          60
His Arg Gly His His His His His His His His His His Glu Glu
  65          70          75          80
Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
      85          90          95
Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Glu Pro Asp Ser
      100        105        110
Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
      115        120        125
Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
      130        135        140
Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
      145        150        155        160
Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Glu Glu Gly Asn
      165        170        175
Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala Phe
      180        185        190
Thr Lys Glu Glu Ile Arg Glu Leu Glu Ala Glu Phe Ala His His Asn
      195        200        205
Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp Leu
      210        215        220
Thr Glu Arg Glu Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp
      225        230        235        240
Lys Arg Val Lys Gly Gly Gln Glu Gly Ala Ala Ala Arg Glu Lys Glu
      245        250        255
Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser Gly
      260        265        270
Ile Gly Ala Ala Thr Leu Gln Glu Thr Gly Asp Ser Ile Ala Asn Glu
      275        280        285
Asp Ser His Asp Ser Asp His Ser Ser Glu His Ala His Leu
      290        295        300

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(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1 i) MOLECULE TYPE: cDNA

(1 i i) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(1 x) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base=1

(1 x) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /mod_base=i

(1 x) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /mod_base=i

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

09755330.010501

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AARATWTGGT TYCARAAYMG WMGWATGAA

29

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: cDNA

(1.1.1) HYPOTHETICAL: NO

(1.v) ANTI-SENSE: YES

(1.x) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /mod_base=1

(x.1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCAWARRTGW GCRTGYTC

18

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: cDNA

(1.1.1) HYPOTHETICAL: NO

(1.v) ANTI-SENSE: NO

(x.1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGCAGAT CTCACTGAAA GACAGGTAAA

30

(2) INFORMATION FOR SEQ ID NO:8:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: cDNA

(1.1.1) HYPOTHETICAL: NO

(1.v) ANTI-SENSE: YES

(x.1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTTACCTGTC TTTCAGTGAG

20

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1.1) MOLECULE TYPE: cDNA

(1.1.1) HYPOTHETICAL: NO

(1.v) ANTI-SENSE: YES

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(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCGCAGAT CTAGATTCAC TGCTATCTCG TA

3 2

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: YES

(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGCGTGCCC CCTCTGATGC TGGCTGGCAA ACATGT

3 6

(2) INFORMATION FOR SEQ ID NO:11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGCGCTCTT GAAGGGCGAG AGAGGATTGG GA

3 2

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG

3 8

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(* 1) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACTTCC AAGGTCTTAG CTATCACTTA AGCAC

3 5

(2) INFORMATION FOR SEQ ID NO:14:

FOUO 0285760

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- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(x 1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGCGCTCG ACGAACACCC CCTCTTTGGC

30

(2) INFORMATION FOR SEQ ID NO:15:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(x 1) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGCAAGC TTTCATAAGT GTGCGTGCTC

30

(2) INFORMATION FOR SEQ ID NO:16:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(x 1) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCGCGCGGC TTTTACATTA GGAGT

25

(2) INFORMATION FOR SEQ ID NO:17:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1 1) MOLECULE TYPE: cDNA

(1 1 1) HYPOTHETICAL: NO

(1 v) ANTI-SENSE: NO

(x 1) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGGCAAAC ATGCCCTCCT CATTG

25

(2) INFORMATION FOR SEQ ID NO:18:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear